AMENDMENTS TO THE SPECIFICATION

Please replace the current title with the rewritten title: -- ~~Novel~~ G Protein Coupled Receptors --.

Please replace the last paragraph on page 19 that extends into page 20 with the following rewritten paragraph as follows:

-- A preferred example of algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al., Nuc. Acids Res.* 25:3389-3402 (1977) and Althschul *et al., J. Mol. Biol* 215: 403-410 (1990), respectively. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information ~~(http://www.ncbi.nlm.nih.gov)~~. This algorithm involves firsts identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al, supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from it s maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the

sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, *Proc. Natl Acad. Sci. USA* 89: 10915 (1989)) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands. --

Please replace the text appearing under the heading Brief Description of the Drawings on page 6 with the following rewritten text as follows:

~~-- Figure 1: Breast cancer tumors and cell lines with amplified copies of the BCA-GPCR-3 gene~~.
~~Figure 2~~ Figure 1: BCA-GPCR-3 mRNA overexpression in breast cancer cell lines.
~~Figure 3: Quantitative data of BCA-GPCR-3 mRNA overexpression in breast cancer cell lines.~~
~~Figure 4~~ Figure 2: BCA-GPCR-3 mRNA overexpression in primary prostate cancer. --

Following the heading Brief Description of the Drawings and the subsequent text, please insert the following new text as follows:

-- BRIEF DESCRIPTION OF THE TABLES

Table 1: Breast cancer tumors and cell lines with amplified copies of the BCA-GPCR-3 gene.
Table 2: Quantitative data of BCA-GPCR-3 mRNA overexpression in breast cancer cell lines. --

Please replace he first paragraph on page 9 with the rewritten paragraph as follows:

-- Structurally, the nucleotide sequence of human BCA-GPCR-3 (*see, e.g.,* SEQ ID NO:5, expressed in placenta and testis) encodes a polypeptide with a predicted molecular weight of approximately 37kDa and a predicted range of 32-42 kDa (*see, e.g.,* SEQ ID NO:6). Related BCA-GPCR-3 genes from other species should share at least

about 70% amino acid identity over a amino acid region at least about 25 amino acids in length, optionally 50 to 100 amino acids in length. BCA-GPCR-3 is amplified at least about 3-7 fold in about 15% of primary breast tumors and tumor cell lines (*see* ~~Figure 1~~ Table 1). In addition, BCA-GPCR-3 mRNA levels are elevated in breast cancer cell lines from both amplified and non-amplified tumors (*see* ~~Figures 2-3~~ Figure 1 and Table 2) --

Please replace the last paragraph on page 59 with the rewritten paragraph as follows:

-- Gene amplification of BCA-GPCR-3 in breast cancer cell lines and tumors was measured according to standard methodology (*see* ~~Figure 1~~ Table 1). BCA-GPCR-3 mRNA expression in breast cancer cell lines was examined using RT-PCR, according to standard methodology (*see* ~~Figures 2-3~~ Figure 1 and Table 2). BCA-GPCR-3 mRNA levels were elevated in cancer cell lines from both amplified and non-amplified tumors, a hallmark of oncogenes. --

Please replace the first paragraph on page 60 with the rewritten paragraph as follows:

-- ~~Figure 4~~ Figure 2 depicts BCA-GPCR-3 mRNA expression in primary prostate cancer. The amount of mRNA expression in was quantified using RT-PCR, according to standard methodology. Briefly, total RNA was isolated from frozen primary breast tumor tissue or from frozen primary prostate tissue using TRIZOL Reagent (GibcoBRL) according to the manufacturer's protocol. Total RNA was treated with DNAaseI (GibcoBRL) to eliminate genomic DNA and reverse transcribed with random primers using cDNA CYCLE KIT (Invitrogen) according to manufacturer's instruction. Following the reverse transcription reaction, PCR was performed for 40 cycles at 94 °C, 45", 58 °C, 45" and 72 °C, 45". --